

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
(Case No. 02-1270-A)

In application of)
J. Fruehauf, *et al.*)
Serial No. 10/734,880)
Filed: December 12, 2003)
For: Gene Related Sensitivity and Resistance)
To Chemotherapeutic Drug Treatment)
Examiner: Lei Yao
Group Art Unit: 1642
Confirmation No.: 1031

Commissioner for Patents
PO Box 1450
Alexandria, VA 22313-14501

RULE 132 DECLARATION OF WILLIAM RICKETTS-
APPENDIX B

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PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Nucleotide** for

Display **GenBank** Show **5** Send to Hide: sequence all but gene, CDS and mRNA features

Range: from **begin** to **end** Reverse complemented strand Features: SNP

1: [AF458589](#). Reports *Homo sapiens* myos...[gi:21360805]

Links

[Features](#) [Sequence](#)

LOCUS AF458589 4631 bp mRNA linear PRI 10-JUN-2002
 DEFINITION Homo sapiens myosin phosphatase target subunit 1 variant (PPP1R12A)
 mRNA, complete cds.
 ACCESSION AF458589
 VERSION AF458589.1 GI:21360805
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 1 (bases 1 to 4631)
 REFERENCE
 AUTHORS Guo, J.H., Chen, X.Y. and Yu, L.
 TITLE Direct Submission
 JOURNAL Submitted (15-DEC-2001) School of Life Sciences, Institute of
 Genetics, Fudan University, Handan Road, 220, Shanghai 200433,
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ORIGIN

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Search for

Display GenBank Show Send to Hide: sequence all but gene, CDS and mRNA features

Range: from to Reverse complemented strand Features:

1: U79283. Reports Human albumin D-b...[gi:1710256]

Links

Features Sequence

LOCUS HSU79283 1480 bp mRNA linear PRI 28-NOV-2000
 DEFINITION Human albumin D-box binding protein mRNA, complete cds.
 ACCESSION U79283
 VERSION U79283.1 GI:1710256
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1480)
 AUTHORS Andersson,B., Wentland,M.A., Ricafrente,J.Y., Liu,W. and Gibbs,R.A.
 TITLE A 'double adaptor' method for improved shotgun library construction
 JOURNAL Anal. Biochem. 236 (1), 107-113 (1996)
 PUBMED 8619474
 REFERENCE 2 (bases 1 to 1480)
 AUTHORS Yu,W., Andersson,B., Worley,K.C., Muzny,D.M., Ding,Y., Liu,W.,
 Ricafrente,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A.
 TITLE Large-scale concatenation cDNA sequencing
 JOURNAL Genome Res. 7 (4), 353-358 (1997)
 PUBMED 9110174
 REFERENCE 3 (bases 1 to 1480)
 AUTHORS Yu,W. and Gibbs,R.A.
 TITLE Direct Submission
 JOURNAL Submitted (22-NOV-1996) Molecular and Human Genetics, Baylor
 College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA
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ORIGIN

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Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Steven Jones, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 141 Row: d Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 45580687.

Differences found between this sequence and the human reference genome (build 36) are described in misc difference features below.

<u>FEATURES</u>	Location/Qualifiers
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<u>gene</u>	1..4015 /gene="C7" /db_xref="GeneID:730" /db_xref="HGNC:1346" /db_xref="MIM:217070"
<u>CDS</u>	96..2627 /gene="C7" /codon_start=1 /product="complement component 7" /protein_id="AAH63851.1" /db_xref="GI:39645843" /db_xref="GeneID:730" /db_xref="HGNC:1346" /db_xref="MIM:217070" /translation="MKVISLFLIVGFIGEFQSFSASSPVNCQWDFYAPWSECNGCTKTQTRRRSRVAVYGQYGGQPCVGNAFETQSCEPTRGCPTEEGCGERFRFCFSQCISKSLSV CNGDSDCDEDESADEDRCEDSERPSCDIDKPPPNIELTGNGYNELTGQFRNRVINTKSGGGQCRKVFGDGKDFYRLSGNVLSYTFQVKINNDFNYEFYNSTWSYVKHTSTEHTSSRKRSSFRSSSSSSRSYTSHTNEIHKGKSQLLVENTVEVAQFINNNPEFLQLAEPFWKEIHLPLSYDYSAYRRLIDQYGTLYLQSGSLGGEYRVLFYVDSEKLKQNDFNSVKEKCKSSGWHFVVFKFSSHGCKELENALKAASGTQNNVLRGEPIFIRGGGAGFISGLSYLEDN PAGNKRRYSAWAESVTNPQVIQKLTPLYELVKEVPCASVKKLYLKWAEEYLD EFDPCCHRPCQNGGLATVEGTHCLCHCKPYTFGAACQGVILVGNQAGGVGDGGWCSWSSWSPCVQGKKTRSRECNNPPPSGGGRSCVGETTESTQCEDEELEHRLILEPHCFPLSLVPTEFCPSPPALKDGFVQDEGTMFPVGKNNVYTCTNEGYSLIGNPVARCGEDLRWLVGENHCQKIACVLPVLMDGIQSHPQKPFYTVGEKVTSCSGGMSLEGPSAFLCGSSLKWSPEMKNARCVQKENPLTQAVPKCQRWEKLQNSRCVKMPYECGPSLVDCAQDERSKRILPTVCKMHVILHCQGRNYTLTGRDSCTL PASAEKACGACPLWGKCDAESSKVCVCREASECEEEGFSICVEVNGKEQTMSCEAGALRCRGQSISVTSIRPCAETQ"
<u>misc difference</u>	3994..4015 /gene="C7" /note="polyA tail: 22 bases do not align to the human genome."

ORIGIN

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 Nucleotide
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PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMM Books
Search for Go Clear
Display Show Send to Hide: sequence all but gene, CDS and mRNA features
Range: from to Reverse complemented strand Features: SNP MGC Refresh

□ 1: BC002788. Reports *Homo sapiens* plas... [gi:33877182]

Order cDNA clone,
Links

Comment Features Sequence

LOCUS BC002788 1353 bp mRNA linear PRI 15-JUL-2006
 DEFINITION Homo sapiens plasminogen activator, urokinase receptor, mRNA (cDNA clone MGC:3905 IMAGE:3617894), complete cds.
 ACCESSION BC002788
 VERSION BC002788.2 GI:33877182
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1353)
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altenschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnurch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 CONSRM Mammalian Gene Collection Program Team
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 1353)
 CONSRM NIH MGC Project
 TITLE Direct Submission
 JOURNAL Submitted (05-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT On Aug 19, 2003 this sequence version replaced gi:[12803884](http://www.ncbi.nlm.nih.gov).
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghghi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 12 Row: j Column: 13

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 53829377.

Differences found between this sequence and the human reference genome (build 36) are described in misc_difference features below.

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<u>CDS</u>	66..1073 /gene="PLAUR" /gene_synonym="UPAR" /gene_synonym="URKR" /gene_synonym="CD87" /codon_start=1 /product="plasminogen activator, urokinase receptor" /protein_id="AAH02788.1" /db_xref="GI:12803885" /db_xref="GeneID:5329" /db_xref="HGNC:9053" /db_xref="MIM:173391" /translation="MGHPPLLPLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQD LCRTTIVRLWEEGEELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGN SGRAVTYSRSRYLECISCGSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGERP KDDRHLRGCGYLPGCPGSNGFHNNDTFHFLKCCTTKCNEGPILELENLPQNNGRQCYS CKGNSTHGSSEETFLIDCRGPMNQCLVATGTPEKNQSYMVRCATASMCQHAHLGD AFSMNHIDVSCTKSGCNHPDLVQYRSGAAPQPGPAHLSLTITLLMTARLWGTTLLW T"
<u>misc_difference</u>	1336..1353 /gene="PLAUR" /gene_synonym="UPAR" /gene_synonym="URKR" /gene_synonym="CD87" /note="polyA tail: 18 bases do not align to the human genome."

ORIGIN

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541 gtccaaagga tgaccggccac ctccgtggct gtggctaccc tccccgtgc cccggctcca

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//

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Last update: Mon, 12 Jan 2009 Rev. 149544

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Search for
Display GenBank Show 5 Send to Hide: sequence all but gene, CDS and mRNA features
Range: from begin to end Reverse complemented strand Features: SNP MGC

1: BC005235. Reports *Homo sapiens* nucl...[gi:13528872]

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Comment Features Sequence

LOCUS BC005235 **1199 bp mRNA linear PRI 15-JUL-2006**
DEFINITION Homo sapiens nuclear DNA-binding protein, mRNA (cDNA clone
MGC:12261 IMAGE:3930648), complete cds.
ACCESSION BC005235
VERSION BC005235.1 GI:13528872
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1199)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnurch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
CONSRTM Mammalian Gene Collection Program Team
TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 1199)
CONSRTM NIH MGC Project
TITLE Direct Submission
JOURNAL Submitted (27-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94301
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 16 Row: 1 Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27894372.

Differences found between this sequence and the human reference genome (build 36) are described in misc_difference features below and these differences were also compared to chimpanzee genome (build 2).

FEATURES	Location/Qualifiers
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/note="polyA tail: 31 bases do not align to the human genome."

ORIGIN

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//

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Last update: Mon, 12 Jan 2009 Rev. 149544

The screenshot shows the NCBI Nucleotide search results for sequence AF237631. At the top, there's a decorative banner with DNA helixes and the NCBI logo. The main search bar has 'Search' set to 'Nucleotide' and 'for' set to 'AF237631'. Below the search bar are buttons for 'Display' (GenBank), 'Show' (5), 'Send to', 'Hide' (checkboxes for sequence and all but gene/CDS/mRNA features), and 'Range' (from 'begin' to 'end'). There are also checkboxes for 'Reverse complemented strand' and 'Features' (SNP). On the right, there are links for 'My NCBI' and '[Sign In] [Register]'.

1: [AF060181](#). Reports Homo sapiens zinc...[gi:3228539]

Links

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LOCUS AF060181 4440 bp mRNA linear PRI 16-JUN-1998
 DEFINITION Homo sapiens zinc finger protein (ZNF198) mRNA, complete cds.
 ACCESSION AF060181
 VERSION AF060181.1 GI:3228539
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 4440)
 AUTHORS Still, I.H. and Cowell, J.K.
 TITLE The t(8;13) atypical myeloproliferative disorder: further analysis
 of the ZNF198 gene and lack of evidence for multiple genes
 disrupted on chromosome 13
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 4440)
 AUTHORS Still, I.H.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-1998) Neurosciences, Cleveland Clinic Foundation,
 9500 Euclid Avenue, Cleveland, OH 44195, USA
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ORIGIN

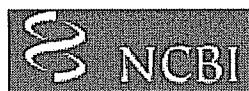
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Range: from **begin** to **end** Reverse complemented strand Features: **[+]** **Refresh**

1: [AF237631](#). Reports Homo sapiens ubiq...[gi:7288860]

Links

Features Sequence

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 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2072)
 AUTHORS Conley,C.A., Almenar-Queralt,A. and Fowler,V.M.
 TITLE Identifying novel tropomodulin isoforms
 JOURNAL Mol. Biol. Cell 9, 18A (1998)
 REFERENCE 2 (bases 1 to 2072)
 AUTHORS Conley,C.A. and Fowler,V.M.
 TITLE Direct Submission
 JOURNAL Submitted (23-FEB-2000) Space Life Sciences, NASA Ames Research Center, M/S 239-11, Moffett Field, CA 94035-1000, USA
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Range: from begin to end Reverse complemented strand Features: SNP

1: D00099. Reports Homo sapiens mRNA...[gi:219941]

Links

Comment Features Sequence

LOCUS HUMNKATPA 4108 bp mRNA linear PRI 11-MAR-1998
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 ACCESSION D00099
 VERSION D00099.1 GI:219941
 KEYWORDS Na,K-ATPase; alpha-subunit.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 4108)
 AUTHORS Kawakami,K., Ohta,T., Nojima,H. and Nagano,K.
 TITLE Primary structure of the alpha-subunit of human Na,K-ATPase deduced
 from cDNA sequence
 JOURNAL J. Biochem. 100 (2), 389-397 (1986)
 PUBMED 2430951
 COMMENT The alpha-subunit of the human Na,K-ATPase exhibited 87% homology
 with its Torpedo counterpart and 98% homology with its sheep
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1: BC002795. Reports Homo sapiens plas...[gi:33877195]

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Comment Features Sequence

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 VERSION BC002795.2 GI:33877195
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 REFERENCE 1 (bases 1 to 2409)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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 CONSRM Mammalian Gene Collection Program Team
 TITLE Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 2409)
 CONSRM NIH MGC Project
 TITLE Direct Submission
 JOURNAL Submitted (05-FEB-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT On Aug 19, 2003 this sequence version replaced gi:12803896.
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghghi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 12 Row: p Column: 15

~~This clone was selected for full length sequencing because it passed the following selection criteria:~~ matched mRNA gi: 14702165.

Differences found between this sequence and the human reference genome (build 36) are described in misc_difference features below.

FEATURES	Location/Qualifiers
source	1..2409 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:3677 IMAGE:3618149" /tissue_type="Skin, melanotic melanoma." /clone_lib="NIH_MGC_20" /lab_host="DH10B-R" /note="Vector: pOTB7"
gene	1..2409 /gene="PLAT" /gene_synonym="TPA" /gene_synonym="T-PA" /db_xref="GeneID:5327" /db_xref="HGNC:9051" /db_xref="MIM:173370"
CDS	84..1634 /gene="PLAT" /gene_synonym="TPA" /gene_synonym="T-PA" /codon_start=1 /product="plasminogen activator, tissue" /protein_id="AAH02795.3" /db_xref="GI:127796397" /db_xref="GeneID:5327" /db_xref="HGNC:9051" /db_xref="MIM:173370" /translation="MDAMKRLCCVLLCGAVFVSPSQEIHARFRGARSYQGCSEPR CFNGGTCCQALYFSDFVCQCPEGFAGKCCEIDTRATCYEDQGISYRGTWSTAESGAEC TNWNSSALAQKPYSGRRPDAIRLGLGNHNYCRNPDRDSKPWCYFKAGKYSSEFCSTP ACSEGNSDCYFGNGSAYRGTHSITESGASCLPWNNSMILIGKVYTAQNPSAQALGLGKH NYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASH PWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPHHLTIVLGRTYRVVP GEQQKFEVEKYIVHKEFDDDTYDNDIALQLKSDSSRCAQESSVVRTVCLPPADQL PDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDT RSGGPQANLHDACQGDGGPLVCLNDGRMTLVGIISWGLGCGQKDVGVTKVNTYLD WIRDNMRP"
misc_difference	2395..2409 /gene="PLAT" /gene_synonym="TPA" /gene_synonym="T-PA" /note="polyA tail: 15 bases do not align to the human genome."

ORIGIN

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2401 aaaaaaaaaa

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